

SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS COMPRISING PROTEIN L IMMUNOGLOBULIN
 BINDING DOMAINS FOR CELL-SPECIFIC TARGETING

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 <151> 2004-04-29

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Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
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Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
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Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu	
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Pro Lys Ala Gly Ser Glu Ala Glu Ile Leu Thr Leu Ala Ala Ala Ser	
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35 40 45

Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
50 55 60

Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
65 70 75 80

Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu

85

90

95

Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
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Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
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Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
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Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
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Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
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Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Lys Glu
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Gln Val Thr Ile Lys Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln
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Thr Ala Thr Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr
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Arg Tyr Ala Asp Leu Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp
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Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly Lys Glu
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Ser Tyr Glu Glu Ala Glu Ala Ala Ala Lys Glu Ala Leu Lys Asn Asp
 485 490 495

Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr
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Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
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Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
 595 600 605

Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr
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Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu
 625 630 635 640

Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
 645 650 655

Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
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Gly Lys Gly Gly Val Asp Ser Pro Lys Lys Lys Glu Lys Ala Ala Leu
 675 680 685

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gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg tat 144
 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
 35 40 45

gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt gca 192
 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
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gat aaa ggt tat act tta aat att aaa ttt gct gga 228
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 20 25 30

Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
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Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
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1 5 10 15

aac tta atc tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga 96
Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
20 25 30

aca ttt gaa gaa gca aca gca gaa gca tac aga tat gca gat gca tta 144
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
35 40 45

aag aag gac aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat 192
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20 25 30

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
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Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
          20          25          30

aca ttt gaa gaa gca aca gca gaa gca tac aga tat gct gac tta tta      144
Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
          35          40          45

gca aaa gaa aat ggt aaa tat aca gta gac gtt gca gat aaa ggt tat      192
Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
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Thr Leu Asn Ile Lys Phe Ala Gly
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Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
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Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
20 25 30

aca ttt gca gaa gca aca gca gaa gca tac aga tac gct gac tta tta 144
Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
35 40 45

gca aaa gaa aat ggt aaa tat aca gca gac tta gaa gat ggt gga tac 192
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20 25 30

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50 55 60

Thr Ile Asn Ile Arg Phe Ala Gly
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 gaa aat ata tat ttt gaa gat gga aca gta caa act gca aca ttt aaa 96
 Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln Thr Ala Thr Phe Lys
 20 25 30
 gga aca ttt gca gaa gcg aca gca gaa gca tac aga tat gca gat ttg 144
 Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu
 35 40 45
 tta tca aaa gaa cat ggt aaa tac aca gca gac ttg gaa gat ggt gga 192
 Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly
 50 55 60
 tac act atc aac att aga ttt gct gga 219
 Tyr Thr Ile Asn Ile Arg Phe Ala Gly
 65 70

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 35 40 45
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 Tyr Thr Ile Asn Ile Arg Phe Ala Gly

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Ser Tyr Cys His His Thr Glu Pro Cys Phe Ser Pro Val Lys Ile Glu	
20 25 30	
cag gtc tgg gac gaa gcg gac gat aac acc ata cgc ata cag act tcc	144
Gln Val Trp Asp Glu Ala Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser	
35 40 45	

gcc cag ttt gga tac gac caa agc gga gca gca agc gca aac aag tac Ala Gln Phe Gly Tyr Asp Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr 50 55 60	192
cgc tac atg tcg ctt gag cag gat cac acc gtt aaa gaa ggc acc atg Arg Tyr Met Ser Leu Glu Gln Asp His Thr Val Lys Glu Gly Thr Met 65 70 75 80	240
gat gac atc aag att agc acc tca gga ccg tgt aga agg ctt agc tac Asp Asp Ile Lys Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Ser Tyr 85 90 95	288
aaa gga tac ttt ctc ctc gca aaa tgc cct cca ggg gac agc gta acg Lys Gly Tyr Phe Leu Leu Ala Lys Cys Pro Pro Gly Asp Ser Val Thr 100 105 110	336
gtt agc ata gtg agt agc aac tca gca acg tca tgt aca ctg gcc cgc Val Ser Ile Val Ser Ser Asn Ser Ala Thr Ser Cys Thr Leu Ala Arg 115 120 125	384
aag ata aaa cca aaa ttc gtg gga cgg gaa aaa tat gat cta cct ccc Lys Ile Lys Pro Lys Phe Val Gly Arg Glu Lys Tyr Asp Leu Pro Pro 130 135 140	432
gtt cac ggt aaa aaa att cct tgc aca gtg tac gac cgt ctg aaa gaa Val His Gly Lys Lys Ile Pro Cys Thr Val Tyr Asp Arg Leu Lys Glu 145 150 155 160	480
aca act gca ggc tac atc act atg cac agg ccg gga ccg cac gct tat Thr Thr Ala Gly Tyr Ile Thr Met His Arg Pro Gly Pro His Ala Tyr 165 170 175	528
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Val Asp Arg Asp Gly Leu Glu Tyr Ile Trp Gly Asn His Glu Pro Val
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His Glu Ile Val Gln His Tyr Tyr His Arg His Pro Val Tyr Thr Ile
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gac gac cac acg gcc caa ggg aaa ttg cat ttg cct ttc aag ttg atc Asp Asp His Thr Ala Gln Gly Lys Leu His Leu Pro Phe Lys Leu Ile 315 320 325	9416
ccg agt acc tgc atg gtc cct gtt gcc cac gcg ccg aat gta ata cat Pro Ser Thr Cys Met Val Pro Val Ala His Ala Pro Asn Val Ile His 330 335 340	9464
ggc ttt aaa cac atc agc ctc caa tta gat aca gac cac ttg aca ttg Gly Phe Lys His Ile Ser Leu Gln Leu Asp Thr Asp His Leu Thr Leu 345 350 355	9512
ctc acc acc agg aga cta ggg gca aac ccg gaa cca acc act gaa tgg Leu Thr Thr Arg Arg Leu Gly Ala Asn Pro Glu Pro Thr Thr Glu Trp 360 365 370	9560
atc gtc gga aag acg gtc aga aac ttc acc gtc gac cga gat ggc ctg Ile Val Gly Lys Thr Val Arg Asn Phe Thr Val Asp Arg Asp Gly Leu 375 380 385 390	9608
gaa tac ata tgg gga aat cat gag cca gtg agg gtc tat gcc caa gag Glu Tyr Ile Trp Gly Asn His Glu Pro Val Arg Val Tyr Ala Gln Glu 395 400 405	9656
tca gca cca gga gac cct cac gga tgg cca cac gaa ata gta cag cat Ser Ala Pro Gly Asp Pro His Gly Trp Pro His Glu Ile Val Gln His 410 415 420	9704
tac tac cat cgc cat cct gtg tac acc atc tta gcc gtc gca tca gct Tyr Tyr His Arg His Pro Val Tyr Thr Ile Leu Ala Val Ala Ser Ala 425 430 435	9752
acc gtg gcg atg atg att ggc gta act gtt gca gtg tta tgt gcc tgt	9800

Thr Val Ala Met Met Ile Gly Val Thr Val Ala Val Leu Cys Ala Cys	
440 445 450	
aaa gcg cgc cgt gag tgc ctg acg cca tac gcc ctg gcc cca aac gcc	9848
Lys Ala Arg Arg Glu Cys Leu Thr Pro Tyr Ala Leu Ala Pro Asn Ala	
455 460 465 470	
gta atc cca act tcg ctg gca ctc ttg tgc tgc gtt agg tcg gcc aat	9896
Val Ile Pro Thr Ser Leu Ala Leu Leu Cys Cys Val Arg Ser Ala Asn	
475 480 485	
gct gaaacgttca ccgagaccat gagttacttg tggtcgaaca gtcagccgtt	9949
Ala	
cttctgggtc cagttgtgca tacctttggc cgctttcatc gttctaatagc gctgctgctc	10009
ctgctgcctg ccttttttag tggttgccgg cgcctacctg gcgaaggtag acgcctacga	10069
acatgcgacc actgttccaa atgtgccaca gataccgtat aaggcacttg ttgaaagggc	10129
agggatatgcc ccgctcaatt tggagatcac tgtcatgtcc toggaggttt tgccttcac	10189
caaccaagag tacattacct gcaaattcac cactgtggtc cctccccaa aaatcaaag	10249
ctgcggctcc ttggaatgtc agccggccgc tcatgcagac tatacctgca aggtcttcgg	10309
aggggtctac ccctttatgt ggggaggagc gcaatgtttt tgcgacagtg agaacagcca	10369
gatgagtgag gcgtacgtcg aattgtcagc agattgcgcg tctgaccacg cgcaggcgat	10429
taaggtgcac actgccgga tgaaagtagg actgcgtatt gtgtacggga aactaccag	10489
tttcctagat gtgtacgtga acggagtcac accaggaacg tctaaagact tgaaagtc	10549
agctggacca atttcagcat cgtttacgcc attcgatcat aaggctcgta tccatgcgg	10609
cctggtgtac aactatgact tcccgaata tggagcgatg aaaccaggag cgtttggaga	10669
cattcaagct acctccttga ctagcaagga tctcatcgcc agcacagaca ttaggtact	10729
caagccttcc gccagaacg tgcattgtcc gtacacgcag gcctcatcag gatttgagat	10789
gtggaaaaac aactcaggcc gccactgca ggaaaccgca ctttcgggt gtaagattgc	10849
agtaaataccg ctccgagcgg tggactgttc atacgggaac attcccattt ctattgacat	10909
cccgaacgct gcctttatca ggacatcaga tgcaccactg gtctcaacag tcaaatgtga	10969
agtcagttag tgcacttatt cagcagactt cggcgggatg gccaccctgc agtatgtatc	11029
cgaccgcgaa ggtcaatgcc ccgtacattc gcattcgagc acagcaactc tccaagagtc	11089
gacagtacat gtcctggaga aaggagcggg gacagtacac tttagcaccg cgagtccaca	11149
ggcgaacttt atcgtatcgc tgtgtgggaa gaagacaaca tgcaatgcag aatgtaaacc	11209

accagctgac catatcgtga gcaccccgca caaaaatgac caagaatttc aagccgcat 11269
ctcaaaaaca tcatggagtt ggctgtttgc ccttttcggc ggcgcctcgt cgctattaat 11329
tataggactt atgatttttg cttgcagcat gatgctgact agcacacgaa gatgaccgct 11389
acgccccaat gatccgacca gcaaaactcg atgtacttcc gaggaactga tgtgcataat 11449
gcatcaggct ggtacattag atccccgctt accgcgggca atatagcaac actaaaaact 11509
cgatgtactt ccgaggaagc gcagtgcata atgctgcgca gtgttgccac ataaccacta 11569
tattaacat ttatctagcg gacgccaaaa actcaatgta tttctgagga agcgtggtgc 11629
ataatgccac gcagcgtctg cataactttt attatttctt ttattaatca acaaaatttt 11689
gtttttaaca tttc 11703

<210> 16
<211> 64
<212> PRT
<213> Sindbis virus

<400> 16

Ser Ala Ala Pro Leu Val Thr Ala Met Cys Leu Leu Gly Asn Val Ser
1 5 10 15

Phe Pro Cys Asp Arg Pro Pro Thr Cys Tyr Thr Arg Glu Pro Ser Arg
20 25 30

Ala Leu Asp Ile Leu Glu Glu Asn Val Asn His Glu Ala Tyr Asp Thr
35 40 45

Leu Leu Asn Ala Ile Leu Arg Cys Gly Ser Ser Gly Arg Ser Lys Arg
50 55 60

<210> 17
<211> 423
<212> PRT
<213> Sindbis virus

<400> 17

Ser Val Ile Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Thr Cys
1 5 10 15

Ser Tyr Cys His His Thr Val Pro Cys Phe Ser Pro Val Lys Ile Glu
20 25 30

Gln Val Trp Asp Glu Ala Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser
 35 40 45
 Ala Gln Phe Gly Tyr Asp Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr
 50 55 60
 Arg Tyr Met Ser Leu Lys Gln Asp His Thr Val Lys Glu Gly Thr Met
 65 70 75 80
 Asp Asp Ile Lys Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Ser Tyr
 85 90 95
 Lys Gly Tyr Phe Leu Leu Ala Lys Cys Pro Pro Gly Asp Ser Val Thr
 100 105 110
 Val Ser Ile Val Ser Ser Asn Ser Ala Thr Ser Cys Thr Leu Ala Arg
 115 120 125
 Lys Ile Lys Pro Lys Phe Val Gly Arg Glu Lys Tyr Asp Leu Pro Pro
 130 135 140
 Val His Gly Lys Lys Ile Pro Cys Thr Val Tyr Asp Arg Leu Lys Glu
 145 150 155 160
 Thr Thr Ala Gly Tyr Ile Thr Met His Arg Pro Arg Pro His Ala Tyr
 165 170 175
 Thr Ser Tyr Leu Glu Glu Ser Ser Gly Lys Val Tyr Ala Lys Pro Pro
 180 185 190
 Ser Gly Lys Asn Ile Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Lys Thr
 195 200 205
 Gly Thr Val Ser Thr Arg Thr Glu Ile Thr Gly Cys Thr Ala Ile Lys
 210 215 220
 Gln Cys Val Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser
 225 230 235 240
 Pro Asp Leu Ile Arg His Asp Asp His Thr Ala Gln Gly Lys Leu His
 245 250 255
 Leu Pro Phe Lys Leu Ile Pro Ser Thr Cys Met Val Pro Val Ala His

260	265	270
Ala Pro Asn Val Ile His Gly Phe Lys His Ile Ser Leu Gln Leu Asp		
275	280	285
Thr Asp His Leu Thr Leu Leu Thr Thr Arg Arg Leu Gly Ala Asn Pro		
290	295	300
Glu Pro Thr Thr Glu Trp Ile Val Gly Lys Thr Val Arg Asn Phe Thr		
305	310	315 320
Val Asp Arg Asp Gly Leu Glu Tyr Ile Trp Gly Asn His Glu Pro Val		
	325	330 335
Arg Val Tyr Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro		
	340	345 350
His Glu Ile Val Gln His Tyr Tyr His Arg His Pro Val Tyr Thr Ile		
	355	360 365
Leu Ala Val Ala Ser Ala Thr Val Ala Met Met Ile Gly Val Thr Val		
	370	375 380
Ala Val Leu Cys Ala Cys Lys Ala Arg Arg Glu Cys Leu Thr Pro Tyr		
385	390	395 400
Ala Leu Ala Pro Asn Ala Val Ile Pro Thr Ser Leu Ala Leu Leu Cys		
	405	410 415
Cys Val Arg Ser Ala Asn Ala		
	420	

<210> 18
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Linker

<220>
 <221> CDS
 <222> (1)..(51)

<400> 18

aga tct ggt ggc ggt ggc tcg ggc ggt ggt ggg tcg ggt ggc ggc gga 48
 Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

tct 51
 Ser

<210> 19
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

<400> 19

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10 15

Ser

<210> 20
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Linker

<220>
 <221> CDS
 <222> (1)..(45)

<400> 20 45
 ggt ggc ggt ggc tcg ggc ggt ggt ggg tcg ggt ggc ggc gga tct
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 21
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic Construct

<400> 21

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1	5	10	15	
<hr/>				
<210>	22			
<211>	1050			
<212>	DNA			
<213>	Bluetongue virus 10			
<hr/>				
<220>				
<221>	CDS			
<222>	(1)..(1050)			
<223>	VP7 gene			
<hr/>				
<400>	22			
atg gac act atc gcc gca aga gca ctc act gtg atg cga gca tgt gct				48
Met Asp Thr Ile Ala Ala Arg Ala Leu Thr Val Met Arg Ala Cys Ala				
1 5 10 15				
acg ctt caa gag gca aga att gtg ttg gaa gcc aat gtg atg gaa att				96
Thr Leu Gln Glu Ala Arg Ile Val Leu Glu Ala Asn Val Met Glu Ile				
20 25 30				
ttg ggg ata gct atc aat agg tac aat gga ctc act tta cga gga gtg				144
Leu Gly Ile Ala Ile Asn Arg Tyr Asn Gly Leu Thr Leu Arg Gly Val				
35 40 45				
acg atg cgc ccg acc tcg tta gca caa aga aat gag atg ttt ttt atg				192
Thr Met Arg Pro Thr Ser Leu Ala Gln Arg Asn Glu Met Phe Phe Met				
50 55 60				
tgt ttg gat atg atg ctg tct gct gct ggg ata aat gtt gga ccg ata				240
Cys Leu Asp Met Met Leu Ser Ala Ala Gly Ile Asn Val Gly Pro Ile				
65 70 75 80				
tcg cca gac tat act caa cat atg gct acg att ggt gta cta gca aca				288
Ser Pro Asp Tyr Thr Gln His Met Ala Thr Ile Gly Val Leu Ala Thr				
85 90 95				
ccg gaa ata cct ttt aca acg gaa gcg gcg aat gaa ata gca cga gtg				336
Pro Glu Ile Pro Phe Thr Thr Glu Ala Ala Asn Glu Ile Ala Arg Val				
100 105 110				
act ggg gag act tcg aca tgg ggg cca gcg cgt cag cct tat ggt ttc				384
Thr Gly Glu Thr Ser Thr Trp Gly Pro Ala Arg Gln Pro Tyr Gly Phe				
115 120 125				
ttc ctt gaa act gag gaa acc ttc caa cca ggg agg tgg ttc atg cgc				432
Phe Leu Glu Thr Glu Glu Thr Phe Gln Pro Gly Arg Trp Phe Met Arg				
130 135 140				
gcc gct caa gca gta act gca gta gtg tgc ggt ccg gat atg att caa				480
Ala Ala Gln Ala Val Thr Ala Val Val Cys Gly Pro Asp Met Ile Gln				
145 150 155 160				
gtg tca cttaaat gct gga gcg aga gga gat gta caa cag ata ttt cag				528
Val Ser Leu Asn Ala Gly Ala Arg Gly Asp Val Gln Gln Ile Phe Gln				

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<210> 22
<211> 1050
<212> DNA
<213> Bluetongue virus 10
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<220>
<221> CDS
<222> (1)..(1050)
<223> VP7 gene
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[illegible]

165										170										175										
ggt	cgt	aat	gat	ccc	atg	atg	ata	tat	tta	gtg	tgg	agg	aga	atc	gaa		576													
Gly	Arg	Asn	Asp	Pro	Met	Met	Ile	Tyr	Leu	Val	Trp	Arg	Arg	Ile	Glu															
			180					185					190																	
aac	ttt	gcg	atg	gcg	caa	ggt	aat	tca	cag	caa	act	caa	gcg	ggt	gtg		624													
Asn	Phe	Ala	Met	Ala	Gln	Gly	Asn	Ser	Gln	Gln	Thr	Gln	Ala	Gly	Val															
		195					200					205																		
act	gtc	agt	gtt	ggt	gga	gtt	gac	atg	agg	gcg	gga	cgc	att	ata	gcg		672													
Thr	Val	Ser	Val	Gly	Gly	Val	Asp	Met	Arg	Ala	Gly	Arg	Ile	Ile	Ala															
	210					215					220																			
tgg	gat	gga	cag	gcc	gcg	ctg	cat	gtg	cat	aat	ccg	aca	caa	cag	aat		720													
Trp	Asp	Gly	Gln	Ala	Ala	Leu	His	Val	His	Asn	Pro	Thr	Gln	Gln	Asn															
	225				230					235					240															
gcg	atg	gtg	caa	ata	cag	gtt	gtg	ttc	tat	ata	tct	atg	gat	aaa	act		768													
Ala	Met	Val	Gln	Ile	Gln	Val	Val	Phe	Tyr	Ile	Ser	Met	Asp	Lys	Thr															
			245					250						255																
tta	aac	cag	tac	ccc	gct	ttg	act	gct	gag	att	ttc	aat	gtt	tac	agc		816													
Leu	Asn	Gln	Tyr	Pro	Ala	Leu	Thr	Ala	Glu	Ile	Phe	Asn	Val	Tyr	Ser															
			260					265					270																	
ttc	agg	gac	cac	aca	tgg	cat	ggg	cta	aga	acg	gcg	ata	tta	aac	aga		864													
Phe	Arg	Asp	His	Thr	Trp	His	Gly	Leu	Arg	Thr	Ala	Ile	Leu	Asn	Arg															
		275					280					285																		
acc	aca	ctg	cca	aac	atg	ctg	cca	cca	atc	ttc	cca	cca	aat	gat	cga		912													
Thr	Thr	Leu	Pro	Asn	Met	Leu	Pro	Pro	Ile	Phe	Pro	Pro	Asn	Asp	Arg															
		290				295					300																			
gat	agc	atc	tta	act	ctt	cta	ctt	tta	tct	aca	ctt	gct	gat	gtt	tac		960													
Asp	Ser	Ile	Leu	Thr	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Ala	Asp	Val	Tyr															
	305				310				315					320																
act	gtt	tta	agg	cca	gag	ttt	gcg	att	cac	ggc	gta	aat	ccg	atg	cca		1008													
Thr	Val	Leu	Arg	Pro	Glu	Phe	Ala	Ile	His	Gly	Val	Asn	Pro	Met	Pro															
			325					330					335																	
ggg	ccg	ctc	aca	cgt	gct	att	gcg	cgc	gcc	gcc	tat	gtg	tag				1050													
Gly	Pro	Leu	Thr	Arg	Ala	Ile	Ala	Arg	Ala	Ala	Tyr	Val																		
			340				345																							

<210> 23
 <211> 349
 <212> PRT
 <213> Bluetongue virus 10

<400> 23

Met	Asp	Thr	Ile	Ala	Ala	Arg	Ala	Leu	Thr	Val	Met	Arg	Ala	Cys	Ala
1				5				10					15		

Thr Leu Gln Glu Ala Arg Ile Val Leu Glu Ala Asn Val Met Glu Ile
 20 25 30

Leu Gly Ile Ala Ile Asn Arg Tyr Asn Gly Leu Thr Leu Arg Gly Val
 35 40 45

Thr Met Arg Pro Thr Ser Leu Ala Gln Arg Asn Glu Met Phe Phe Met
 50 55 60

Cys Leu Asp Met Met Leu Ser Ala Ala Gly Ile Asn Val Gly Pro Ile
 65 70 75 80

Ser Pro Asp Tyr Thr Gln His Met Ala Thr Ile Gly Val Leu Ala Thr
 85 90 95

Pro Glu Ile Pro Phe Thr Thr Glu Ala Ala Asn Glu Ile Ala Arg Val
 100 105 110

Thr Gly Glu Thr Ser Thr Trp Gly Pro Ala Arg Gln Pro Tyr Gly Phe
 115 120 125

Phe Leu Glu Thr Glu Glu Thr Phe Gln Pro Gly Arg Trp Phe Met Arg
 130 135 140

Ala Ala Gln Ala Val Thr Ala Val Val Cys Gly Pro Asp Met Ile Gln
 145 150 155 160

Val Ser Leu Asn Ala Gly Ala Arg Gly Asp Val Gln Gln Ile Phe Gln
 165 170 175

Gly Arg Asn Asp Pro Met Met Ile Tyr Leu Val Trp Arg Arg Ile Glu
 180 185 190

Asn Phe Ala Met Ala Gln Gly Asn Ser Gln Gln Thr Gln Ala Gly Val
 195 200 205

Thr Val Ser Val Gly Gly Val Asp Met Arg Ala Gly Arg Ile Ile Ala
 210 215 220

Trp Asp Gly Gln Ala Ala Leu His Val His Asn Pro Thr Gln Gln Asn
 225 230 235 240

Ala Met Val Gln Ile Gln Val Val Phe Tyr Ile Ser Met Asp Lys Thr
245 250 255

Leu Asn Gln Tyr Pro Ala Leu Thr Ala Glu Ile Phe Asn Val Tyr Ser
260 265 270

Phe Arg Asp His Thr Trp His Gly Leu Arg Thr Ala Ile Leu Asn Arg
275 280 285

Thr Thr Leu Pro Asn Met Leu Pro Pro Ile Phe Pro Pro Asn Asp Arg
290 295 300

Asp Ser Ile Leu Thr Leu Leu Leu Leu Ser Thr Leu Ala Asp Val Tyr
305 310 315 320

Thr Val Leu Arg Pro Glu Phe Ala Ile His Gly Val Asn Pro Met Pro
325 330 335

Gly Pro Leu Thr Arg Ala Ile Ala Arg Ala Ala Tyr Val
340 345

<210> 24
<211> 585
<212> DNA
<213> Coccidioides immitis

<220>
<221> CDS
<222> (1)..(585)
<223> Ag2/PRA gene

<400> 24
atg cag ttc tct cac gct ctc atc gct ctc gtc gct gcc ggc ctc gcc 48
Met Gln Phe Ser His Ala Leu Ile Ala Leu Val Ala Ala Gly Leu Ala
1 5 10 15
agt gcc cag ctc cca gac atc cca cct tgc gct ctc aac tgc ttc gtt 96
Ser Ala Gln Leu Pro Asp Ile Pro Pro Cys Ala Leu Asn Cys Phe Val
20 25 30
gag gct ctc ggc aac gat ggc tgc act cgc ttg acc gac ttc aag tgc 144
Glu Ala Leu Gly Asn Asp Gly Cys Thr Arg Leu Thr Asp Phe Lys Cys
35 40 45
cac tgc tcc aag cct gag cta cca gga cag atc act cct tgc gtt gag 192
His Cys Ser Lys Pro Glu Leu Pro Gly Gln Ile Thr Pro Cys Val Glu
50 55 60
gag gcc tgc cct ctc gac gcc cgt atc tcc gtc tcc aac atc gtc gtt 240

Glu	Ala	Cys	Pro	Leu	Asp	Ala	Arg	Ile	Ser	Val	Ser	Asn	Ile	Val	Val		
65					70					75					80		
gac cag tgc tcc aag gcc ggt gtc cca att gac atc cca cca gtt gac																	288
Asp Gln Cys Ser Lys Ala Gly Val Pro Ile Asp Ile Pro Pro Val Asp																	
				85					90						95		
acc acc gcc gct ccc gag cca tcc gag acc gct gag ccc acc gct gag																	336
Thr Thr Ala Ala Pro Glu Pro Ser Glu Thr Ala Glu Pro Thr Ala Glu																	
				100					105						110		
cca acc gag gag ccc act gcc gag cct acc gct gag ccc acc gct gag																	384
Pro Thr Glu Glu Pro Thr Ala Glu Pro Thr Ala Glu Pro Thr Ala Glu																	
				115					120						125		
ccg act cat gag ccc acc gag gag ccc act gcc gtc cca acc ggc act																	432
Pro Thr His Glu Pro Thr Glu Glu Pro Thr Ala Val Pro Thr Gly Thr																	
				130					135						140		
ggc ggt ggt gtc ccc act ggc acc ggt tcc ttc acc gtc act ggc aga																	480
Gly Gly Gly Val Pro Thr Gly Thr Gly Ser Phe Thr Val Thr Gly Arg																	
				145					150						155		160
cca act gcc tcc acc cca gct gag ttc cca ggt gct ggc tcc aac gtc																	528
Pro Thr Ala Ser Thr Pro Ala Glu Phe Pro Gly Ala Gly Ser Asn Val																	
				165					170						175		
cgt gcc agc gtt ggc ggc att gct gct gct ctc ctc ggt ctc gct gcc																	576
Arg Ala Ser Val Gly Gly Ile Ala Ala Ala Leu Leu Gly Leu Ala Ala																	
				180					185						190		
tac ctg taa																	585
Tyr Leu																	

<210> 25
 <211> 194
 <212> PRT
 <213> *Coccidioides immitis*

<400> 25

Met	Gln	Phe	Ser	His	Ala	Leu	Ile	Ala	Leu	Val	Ala	Ala	Gly	Leu	Ala		
1				5					10					15			

Ser	Ala	Gln	Leu	Pro	Asp	Ile	Pro	Pro	Cys	Ala	Leu	Asn	Cys	Phe	Val		
			20					25					30				

Glu	Ala	Leu	Gly	Asn	Asp	Gly	Cys	Thr	Arg	Leu	Thr	Asp	Phe	Lys	Cys		
		35				40						45					

His	Cys	Ser	Lys	Pro	Glu	Leu	Pro	Gly	Gln	Ile	Thr	Pro	Cys	Val	Glu		
	50					55					60						

Glu Ala Cys Pro Leu Asp Ala Arg Ile Ser Val Ser Asn Ile Val Val
65 70 75 80

Asp Gln Cys Ser Lys Ala Gly Val Pro Ile Asp Ile Pro Pro Val Asp
85 90 95

Thr Thr Ala Ala Pro Glu Pro Ser Glu Thr Ala Glu Pro Thr Ala Glu
100 105 110

Pro Thr Glu Glu Pro Thr Ala Glu Pro Thr Ala Glu Pro Thr Ala Glu
115 120 125

Pro Thr His Glu Pro Thr Glu Glu Pro Thr Ala Val Pro Thr Gly Thr
130 135 140

Gly Gly Gly Val Pro Thr Gly Thr Gly Ser Phe Thr Val Thr Gly Arg
145 150 155 160

Pro Thr Ala Ser Thr Pro Ala Glu Phe Pro Gly Ala Gly Ser Asn Val
165 170 175

Arg Ala Ser Val Gly Gly Ile Ala Ala Ala Leu Leu Gly Leu Ala Ala
180 185 190

Tyr Leu

<210> 26
<211> 906
<212> DNA
<213> Streptococcus pneumoniae

<220>
<221> CDS
<222> (1)..(906)
<223> PspA gene

<400> 26
gaa gaa tct ccc gta gcc agt cag tct aaa gct gag aaa gac tat gat 48
Glu Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp
1 5 10 15

gca gcg aag aaa gat gct aag aat gcg aaa aaa gca gta gaa gat gct 96
Ala Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala
20 25 30

caa aag gct tta gat gat gca aaa gct gct cag aaa aaa tat gac gag Gln Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu 35 40 45	144
gat cag aag aaa act gag gag aaa gcc gcg cta gaa aaa gca gcg tct Asp Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser 50 55 60	192
gaa gag atg gat aag gca gtg gca gca gtt caa caa gcg tat cta gcc Glu Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala 65 70 75 80	240
tat caa caa gct aca gac aaa gcc gca aaa gac gca gca gat aag atg Tyr Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met 85 90 95	288
ata gat gaa gct aag aaa cgc gaa gaa gag gca aaa act aaa ttt aat Ile Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn 100 105 110	336
act gtt cga gca atg gta gtt cct gag cca gag cag ttg gct gag act Thr Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr 115 120 125	384
aag aaa aaa tca gaa gaa gct aaa caa aaa gca cca gaa ctt act aaa Lys Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys 130 135 140	432
aaa cta gaa gaa gct aaa gca aaa tta gaa gag gct gag aaa aaa gct Lys Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala 145 150 155 160	480
act gaa gcc aaa caa aaa gtg gat gct gaa gaa gtc gct cct caa gct Thr Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala 165 170 175	528
aaa atc gct gaa ttg gaa aat caa gtt cat aga cta gaa caa gag ctc Lys Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu 180 185 190	576
aaa gag att gat gag tct gaa tca gaa gat tat gct aaa gaa ggt ttc Lys Glu Ile Asp Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe 195 200 205	624
cgt gct cct ctt caa tct aaa ttg gat gcc aaa aaa gct aaa cta tca Arg Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser 210 215 220	672
aaa ctt gaa gag tta agt gat aag att gat gag tta gac gct gaa att Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile 225 230 235 240	720
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Glu Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys	
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Ala Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu	
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Gln Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu
35 40 45

Asp Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser
50 55 60

Glu Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala
65 70 75 80

Tyr Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met
85 90 95

Ile Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn
100 105 110

Thr Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr
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Lys Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys
130 135 140

Lys Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala

145		150		155		160									
Thr	Glu	Ala	Lys	Gln	Lys	Val	Asp	Ala	Glu	Glu	Val	Ala	Pro	Gln	Ala
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Lys	Ile	Ala	Glu	Leu	Glu	Asn	Gln	Val	His	Arg	Leu	Glu	Gln	Glu	Leu
			180					185						190	
Lys	Glu	Ile	Asp	Glu	Ser	Glu	Ser	Glu	Asp	Tyr	Ala	Lys	Glu	Gly	Phe
		195					200						205		
Arg	Ala	Pro	Leu	Gln	Ser	Lys	Leu	Asp	Ala	Lys	Lys	Ala	Lys	Leu	Ser
	210					215					220				
Lys	Leu	Glu	Glu	Leu	Ser	Asp	Lys	Ile	Asp	Glu	Leu	Asp	Ala	Glu	Ile
225					230					235					240
Ala	Lys	Leu	Glu	Asp	Gln	Leu	Lys	Ala	Ala	Glu	Glu	Asn	Asn	Asn	Val
				245					250						255
Glu	Asp	Tyr	Phe	Lys	Glu	Gly	Leu	Glu	Lys	Thr	Ile	Ala	Ala	Lys	Lys
			260					265						270	
Ala	Glu	Leu	Glu	Lys	Thr	Glu	Ala	Asp	Leu	Lys	Lys	Ala	Val	Asn	Glu
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Pro	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Thr	Pro	Ala	Pro	Glu		
	290					295					300				